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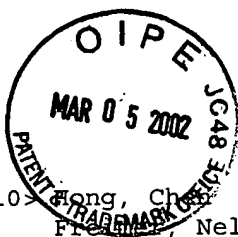
<110> Hong, Chen
       Freimer, Nelson B.

<120> METHODS OF DIAGNOSING NEUROPSYCHIATRIC DISORDERS

<130> 07334-362001

<140> 09/722,544
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tgtgccctcg gctgacttcc agccggtggc acagacgcct ccaggggggca gcactcaagc   120
gcatcttagg aatgacagag ttgcgtccct ctctgttgcc aggctggagt tcagtggcat   180
gttcttagct cactgaagcc tcaaattcct gggttcaagt gaccctccca cctcagcccc   240
atgaggacct gggactacag gacacagcta aatccctgac acgg atg aaa att aaa   296
                                                   Met Lys Ile Lys
                                                    1

gca gag aaa aac gaa ggt cct tcc aga agc tgg tgg caa ctt cac tgg   344
Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His Trp
 5   10   15   20

gga gat att gca aat aac agc ggg aac atg aag ccg cca ctc ttg gtg   392
Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu Val
                25   30   35

ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca ccc act   440
Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro Thr
                40   45   50

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tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt tct gag      488
Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser Glu
            55                  60                  65

gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg act ggt      536
Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr Gly
            70                  75                  80

att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa cac acc      584
Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His Thr
85                  90                  95                 100

aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag gag gcc      632
Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala
                105                 110                 115

ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa gaa agg      680
Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu Arg
                120                 125                 130

cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg tct tgc      728
Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys
                135                 140                 145

ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct agc tgg      776
Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser Trp
150                 155                 160

tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata tat caa      824
Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile Tyr Gln
165                 170                 175                 180

ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc atc agt      872
Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro Ile Ser
                185                 190                 195

gaa aag ctc att gag gaa gat gca caa ttg acc caa atg gag gat gtg      920
Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu Asp Val
                200                 205                 210

ttc agc cag ttg act gtg gat gtg aat tct ctc ttt aac agg agt ttt      968
Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg Ser Phe
                215                 220                 225

aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt caa tca     1016
Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe Gln Ser
                230                 235                 240

cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt cca gct     1064
His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe Pro Ala
245                 250                 255                 260

ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt tgg gac     1112
Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys Trp Asp
                265                 270                 275
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att ccc aac ttc ttc cag ctg ttt tgt aat ttc agt gtc tct att tat        1160
Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser Ile Tyr
            280                 285                 290

gaa agt gtc agt gaa aca att act aag atg ctg aag gca ata gaa gat        1208
Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile Glu Asp
            295                 300                 305

tta cca aaa caa gac aaa gct cct gac cac gga ggc ctg att tca aag        1256
Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile Ser Lys
            310                 315                 320

atg tta cct ggg cag gac aga gga ctg tgt ggg gaa ctt gac cag aat        1304
Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp Gln Asn
325                 330                 335                 340

ttg tca aga tgt ttc aaa ttt cat gaa aaa tgc caa aaa tgt cag gct        1352
Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys Gln Ala
                345                 350                 355

cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca gaa tta        1400
His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr Glu Leu
                360                 365                 370

gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat ggc cag        1448
Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr Gly Gln
            375                 380                 385

att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat ctg gtg        1496
Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr Leu Val
            390                 395                 400

gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca aac cag        1544
Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala Asn Gln
405                 410                 415                 420

gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt cca agg        1592
Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val Pro Arg
                425                 430                 435

att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg aca gac        1640
Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met Thr Asp
                440                 445                 450

tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct ctt gaa        1688
Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro Leu Glu
                455                 460                 465

gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca aaa gct        1736
Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala Lys Ala
            470                 475                 480

cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc taatgcatcc     1789
Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
485                 490                 495

tatatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga aataaaaaag     1849
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gataatgcaa taaacacagt tgcaggaaag tatgttagct atatactatg aagtactctt   1909
agtttactta tgttgaatgg cttagctatt aatactcaaa ttgagttaaa atgaaaattc   1969
ctccttaaaa aatcaaacgt aatatgtatt acatttcatg gtacattagt agttctttgt   2029
atattgaata aatactaaat caccta                                        2055
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<212> PRT
<213> Homo sapiens

<400> 2

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Gln Leu His Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro
            20                  25                  30
Pro Leu Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His
        35                  40                  45
Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys
    50                  55                  60
Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys
65                  70                  75                  80
Ala Leu Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu
                85                  90                  95
Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu
            100                 105                 110
Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu
        115                 120                 125
Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu
    130                 135                 140
Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys
145                 150                 155                 160
Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg
                165                 170                 175
Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp
            180                 185                 190
Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln
        195                 200                 205
Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe
    210                 215                 220
Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln
225                 230                 235                 240
Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr
                245                 250                 255
Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu
            260                 265                 270
Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser
        275                 280                 285
Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys
    290                 295                 300
Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly
305                 310                 315                 320
Leu Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu
                325                 330                 335
Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln
            340                 345                 350
Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu
        355                 360                 365
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```
His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln
    370             375             380
Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr
385             390             395             400
Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu
            405             410             415
Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln
            420             425             430
Val Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr
            435             440             445
Met Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys
    450             455             460
Ile Pro Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val
465             470             475             480
Val Ala Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
            485             490             495
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<213> Homo sapiens

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gcatcttagg aatgacagag ttgcgtccct ctckgttgcc aggctggagt tcagtggcat   180
gttcwtagct cactgaagcc tcaaattcct gggttcaagt gaccctccya cctcagcccc   240
atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc      288
Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu
 1               5                  10                  15

ttg gtg ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca     336
Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala
                20                  25                  30

ccc act tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt     384
Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe
            35                  40                  45

tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg     432
Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu
        50                  55                  60

act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa     480
Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu
65                  70                  75                  80

cac acc aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag     528
His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln
                85                  90                  95

gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa     576
Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu
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                100                    105                    110

gaa agg cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg        624
Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg
        115                    120                    125

tct tgc ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct        672
Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro
        130                    135                    140

agc tgg tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata        720
Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile
145                    150                    155                    160

tat caa ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc        768
Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro
                    165                    170                    175

atc agt gaa aag ctc att gag gaa gat gca caa ttg acc caa atg gag        816
Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu
                180                    185                    190

gat gtg ttc agc cag ttg act gtg gat gtg aat tct ctc ttt aac agg        864
Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg
        195                    200                    205

agt ttt aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt        912
Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe
        210                    215                    220

caa tca cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt        960
Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe
225                    230                    235                    240

cca gct ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt       1008
Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys
                    245                    250                    255

tgg gac att ccc aac ttc ttc cag ctg ttt tgt aat ttc agt gtc tct       1056
Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser
                    260                    265                    270

att tat gaa agt gtc agt gaa aca att act aag atg ctg aag gca ata       1104
Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile
                275                    280                    285

gaa gat tta cca aaa caa gac aaa gct cct gac cac gga ggc ctg att       1152
Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile
        290                    295                    300

tca aag atg tta cct ggg cag gac aga gga ctg tgt ggg gaa ctt gac       1200
Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp
305                    310                    315                    320

cag aat ttg tca aga tgt ttc aaa ttt cat gaa aaa tgc caa aaa tgt       1248
Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys
                325                    330                    335
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cag gct cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca    1296
Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr
            340             345             350

gaa tta gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat    1344
Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr
            355             360             365

ggc cag att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat    1392
Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr
            370             375             380

ctg gtg gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca    1440
Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala
385             390             395             400

aac cag gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt    1488
Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val
                405             410             415

cca agg att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg    1536
Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met
                420             425             430

aca gac tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct    1584
Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro
            435             440             445

ctt gaa gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca    1632
Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala
    450             455             460

aaa gct cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc    1681
Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
465             470             475


taatgcatcc tatatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga  1741
aataaaaaag gataatgcaa taaacacagt tgcaggaaag tatgttagct atatactatg  1801
aagtactctt agtttactta tgttgaatgg cttagctatt aatactcaaa ttgagttaaa  1861
atgaaaattc ctccttaaaa aatcaaacgt aatatgtatt acatttcatg gtacattagt  1921
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<212> PRT
<213> Homo sapiens

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            20              25              30
Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe
        35              40              45
Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu
    50              55              60
```

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Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu
65              70              75              80
His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln
                85              90              95
Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu
            100             105             110
Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg
        115             120             125
Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro
    130             135             140
Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile
145             150             155             160
Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro
            165             170             175
Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu
        180             185             190
Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg
        195             200             205
Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe
    210             215             220
Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe
225             230             235             240
Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys
            245             250             255
Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser
        260             265             270
Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile
    275             280             285
Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile
    290             295             300
Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp
305             310             315             320
Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys
            325             330             335
Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr
            340             345             350
Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr
        355             360             365
Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr
    370             375             380
Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala
385             390             395             400
Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val
            405             410             415
Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met
        420             425             430
Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro
        435             440             445
Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala
    450             455             460
Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
465             470             475
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<212> DNA
<213> Homo sapiens

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ctgctgtggt tgaaagacag tcactgcgca cccacttgga aggacaaaac tgctatcagt     180
gaaaacctga agagtttttc tgaggtgggg gagatagatg cagatgaaga ggtgaagaag     240
gctttgactg gtattaagca aatgaaaatc atgatggaaa gaaaagagaa ggaacacacc     300
aatctaatga gcaccctgaa gaaatgcaga gaagaaaagc aggaggccct gaaacttctg     360
aatgaagttc aagaacatct ggaggaagaa gaaaggctat gccgggagtc tttggcagat     420
tcctggggtg aatgcaggtc ttgcctggaa ataactgca tgagaattta tacaacctgc      480
caacctagct ggtcctctgt gaaaaataag attgaacggt ttttcaggaa gatatatcaa     540
tttctatttc ctttccatga agataatgaa aaagatctcc ccatcagtga aaagctcatt     600
gaggaagatg cacaattgac ccaaatggag gatgtgttca gccagttgac tgtggatgtg     660
aattctctct ttaacaggag ttttaacgtc ttcagacaga tgcagcaaga gtttgaccag     720
acttttcaat cacatttcat atcagataca gacctaactg agccttactt ttttccagct     780
ttctctaaag agccgatgac aaaaagcagat cttgagcaat gttgggacat tcccaacttc     840
ttccagctgt tttgtaattt cagtgtctct atttatgaaa gtgtcagtga acaattact      900
aagatgctga aggcaataga agatttacca aaacaagaca aagctcctga ccacggaggc     960
ctgatttcaa agatgttacc tgggcaggac agaggactgt gtggggaact tgaccagaat    1020
ttgtcaagat gtttcaaatt tcatgaaaaa tgccaaaaat gtcaggctca cctatctgaa    1080
gactgtcctg atgtacctgc tctgcacaca gaattagacg aggcgatcag gttggtcaat    1140
gtatccaatc agcagtatgg ccagattctc cagatgaccc ggaagcactt ggaggacacc    1200
gcctatctgg tggagaagat gagagggcaa tttggctggg tgtctgaact ggcaaaccag    1260
gccccagaaa cagagatcat ctttaattca atacaggtag ttccaaggat tcatgaagga    1320
aatatttcca aacaagatga aacaatgatg acagacttaa gcattctgcc ttcctctaat    1380
ttcacactca agatccctct tgaagaaagt gctgagagtt ctaacttcat tggctacgta    1440
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<210> 6
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<212> DNA
<213> Homo sapiens

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